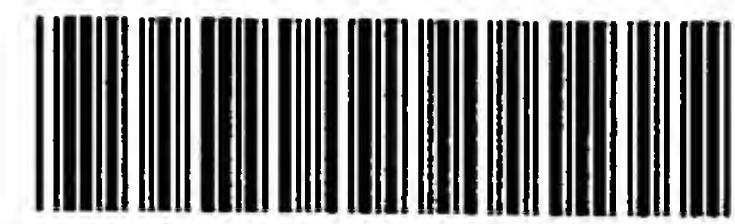


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591, 248
Source: IFWP
Date Processed by STIC: 09/12/2006

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IFWP

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PATENT APPLICATION: US/10/591,248

DATE: 09/12/2006

TIME: 11:33:48

Input Set : A:\Q96497 Sequence Listing.txt

Output Set: N:\CRF4\09122006\J591248.raw

3 <110> APPLICANT: Kaneka Corp.
 4 OKUBO, Yuji
 5 MATSUMOTO, Keiji
 6 TAKAGI, Masamichi
 7 OHTA, Akinori
 9 <120> TITLE OF INVENTION: NOVEL TRANSFORMANT AND PROCESS FOR PRODUCING POLYESTER USING
 THE

10 SAME
 12 <130> FILE REFERENCE: Q96497
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/591,248
 C--> 14 <141> CURRENT FILING DATE: 2006-08-31
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003589
 15 <151> PRIOR FILING DATE: 2005-03-03
 17 <150> PRIOR APPLICATION NUMBER: JP 2004-061291
 18 <151> PRIOR FILING DATE: 2004-03-04
 20 <150> PRIOR APPLICATION NUMBER: JP 2004-062812
 21 <151> PRIOR FILING DATE: 2004-03-05
 23 <160> NUMBER OF SEQ ID NOS: 39
 25 <170> SOFTWARE: PatentIn version 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 102
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: chemically-synthesized restriction enzyme cleavage site
 35 <400> SEQUENCE: 1
 36 aagctgcggc cgcaagttgc atgcctgcag gtcgactcta gaggatcctc gaggatcccc 60
 38 gggtacgcta gcgtaccgag ctatccattt aaatccgaat tc 102
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 1785
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: chemically-synthesized polynucleotide encoding mutant

Aeromonas

48 caviae phaC having mutation at codon 149
 50 <400> SEQUENCE: 2
 51 atgtctcaac catcttatgg tccattgttc gaagctttgg ctcattacaa tgataaattg 60
 53 ttggctatgg ctaaagctca aaccgaaaga actgctcaag ccttgttgca aactaacttg 120
 55 gatgatttgg gtcaagtttt ggaacaaggt tctcaacaac catggcaatt gattcaagct 180
 57 caaatgaatt ggtggcaaga tcaattaaaa ttgatgcaac acactttgtt aaaatctgct 240
 59 ggtcaaccat ctgaaccagt tattactcca gaaagatctg atagaagatt taaagctgaa 300
 61 gcttggtctg aacaaccaat ttatgattac ttaaaacaat cctatttgg aactgctaga 360
 63 cattgttgg cttctgttga tgctttggaa ggtgtcccac aaaaatctag agaaagattg 420

65 agattcttta ctagacaata cgtctccgct atggctccat ctaatttctt ggctactaac 480

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67 ccagaattgt	taaaattgac	tttggaatcc	gatggtaaaa	atttggtag	aggttggct	540
69 ttattggctg	aagatttgg	aagatctgct	gatcaattaa	acattagatt	gactgatgaa	600
71 tccgcctttg	aattaggtag	agatttggct	ttgactccag	gtagagttgt	tcaaagaact	660
73 gaattatatg	aattaattca	atactctcca	actactgaaa	ccgttggtaa	aaccccaagtt	720
75 ttgatcggtc	caccattcat	taataaatat	tacattatgg	atatgagacc	acaaaactcc	780
77 ttggcgctt	ggttggtcgc	tcaaggtcaa	accgtttca	tgatttcctg	gagaaaccca	840
79 ggtgttgctc	aagctcaaat	tgatttagat	gattatgtt	ttgatgggt	cattgctgt	900
81 ttggatggtg	ttgaagccgc	tactggtaa	agagaagttc	acggatttgg	ttactgtatt	960
83 ggtggtaccg	ctttgtctt	agctatgggt	tggttggccg	ccagaagaca	aaaacaaaga	1020
85 gttagaactg	ctactttgtt	tactacttt	ttggatttct	cccaaccagg	tgaattgggt	1080
87 attttatttc	atgaaccaat	tatcgccgcc	ttagaagccc	aaaatgaagc	taaaggtatt	1140
89 atggatggta	gacaattggc	cgtctccttc	tctttgttga	gagaaaactc	tttatattgg	1200
91 aattactata	ttgattctta	cttaaaaggt	caatctccag	ttgctttga	tttgttgcac	1260
93 tggaaactctg	attctactaa	tgttgcgg	aaaactcata	actctttgtt	gagaagattta	1320
95 tatttggaaa	atcaattgg	taaaggtgaa	ttaaaaatta	gaaacactag	aattgattta	1380
97 ggtaaagtt	aaactccagt	tttgggtt	tctgccgtt	atgatcacat	tgctttatgg	1440
99 caaggtacct	ggcaaggtat	gaaatttttc	gggtgtgaac	aaagatttt	attggccgaa	1500
101 tccggtcata	ttgctggat	tattaatcca	ccagctgcta	acaaatacgg	tttctggcac	1560
103 aatggtgctg	aagctgaatc	tccagaatct	tggttggctg	gtgccaccca	tcaaggttgt	1620
105 tcctggtggc	cagaaatgt	gggtttatt	caaaacagag	atgaaggttc	tgaaccagtc	1680
107 ccagccagag	tcccagaaga	aggttggct	ccagctccag	gtcactatgt	caaagttaga	1740
109 ttaaaccag	tttcgctt	tccaaccgaa	gaagatgctg	cttaa		1785
112 <210>	SEQ ID NO:	3				
113 <211>	LENGTH:	741				
114 <212>	TYPE:	DNA				
115 <213>	ORGANISM:	Artificial Sequence				
117 <220>	FEATURE:					
118 <223>	OTHER INFORMATION:	chemically synthesized polynucleotide encoding Ralstonia				
eutropha						
119	phbB for expression in	Candida maltosa				
121 <400>	SEQUENCE:	3				
122 atgactcaaa	gaattgccta	cgttactgg	ggtatgggt	gtattggta	tgctattt	60
124 caaagattgg	ctaaagatgg	tttagagtt	gttgctgg	gtggccaaa	ctctccaaga	120
126 agagaaaaat	ggttggaca	acaaaaagct	ttgggttcg	attttattgc	ttctgaaggt	180
128 aatgttgctg	attgggattc	tactaaaact	gcttcgata	aagtcaaatc	cgaagtcggt	240
130 gaagttgatg	tttgattaa	caatgctgtt	attactagag	atgttggttt	tagaaaaatg	300
132 actagagctg	attgggatgc	cgttattt	actaacttga	cttctttgtt	caatgtcact	360
134 aaacaagtta	ttgatggat	ggctgataga	ggttgggt	gaattgtcaa	catttcttct	420
136 gttaatggtc	aaaaaggtca	atttggtcaa	actaactatt	ccactgctaa	agctggttt	480
138 catggtttca	ctatggctt	ggcccaagaa	gttgcacta	aaggtgttac	tgtcaatacc	540
140 gtctctccag	gttacattgc	tactgatatg	gtcaaagcca	ttagacaaga	tgttttagat	600
142 aaaattgtcg	ccaccattcc	agtcaaaaga	ttgggttgc	cagaagaaat	tgcttctatt	660
144 tgtgcttgg	tgtcttctga	agaatccgtt	tttctactg	gtgctgattt	ctctttaaac	720
146 ggtggtttgc	acatgggtt	a				741
149 <210>	SEQ ID NO:	4				
150 <211>	LENGTH:	754				
151 <212>	TYPE:	DNA				
152 <213>	ORGANISM:	Artificial Sequence				
154 <220>	FEATURE:					
155 <223>	OTHER INFORMATION:	chemically-synthesized promoter with multiple alkane				
responsible						

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156 regions

158 <400> SEQUENCE: 4

159	aagcttgc	gcctgcagg	cgaaattcga	gctcggtacc	cggggatcct	ctagagtcca	60
161	tgtgctttt	ttttgtttt	caatttgaaa	gttttttat	ttccgcaata	caaaattatt	120
163	tttatccgc	tcatgtgctt	tttttttgt	tttcaatttgc	aaagttttt	tatttccgca	180
165	atacaaaatt	atttttatac	cgctgaccca	gatcctctag	agtccatgtg	ctttttttt	240
167	tgtttcaat	ttgaaagttt	tttatttcc	gcaatacaaa	attattttt	atccgctcat	300
169	gtgctttttt	ttttgttttc	aatttgaaaag	tttttttatt	tccgcaatac	aaaattattt	360
171	tttatccgct	gaccagatc	ctctagagtc	catgtgctt	tttttttgtt	ttcaatttga	420
173	aagttttttt	attccgcaa	tacaaaatta	tttttatcc	gctcatgtgc	ttttttttt	480
175	gttttcaatt	tgaaagttt	tttatttccg	caatacaaaa	ttattttta	tccgctgacc	540
177	cagatctcga	ctctagagga	tccccgtttt	tttatttccg	caatacaaaa	ttattttta	600
179	tccgctttcc	gttcctttct	tcttgtgata	aatctcaaca	attatataata	tcattccata	660
181	accctgaata	attttttttt	taagtccttg	gtttctttt	ttagaaaaaa	aggtgaatca	720
183	gtaaaatttt	tgttatttat	catttaact	caca			754

186 <210> SEQ ID NO: 5

187 <211> LENGTH: 594

188 <212> TYPE: PRT

189 <213> ORGANISM: Aeromonas caviae

191 <400> SEQUENCE: 5

193 Met Ser Gln Pro Ser Tyr Gly Pro Leu Phe Glu Ala Leu Ala His Tyr

194 1 5 10 15

197 Asn Asp Lys Leu Leu Ala Met Ala Lys Ala Gln Thr Glu Arg Thr Ala

198 20 25 30

201 Gln Ala Leu Leu Gln Thr Asn Leu Asp Asp Leu Gly Gln Val Leu Glu

202 35 40 45

205 Gln Gly Ser Gln Gln Pro Trp Gln Leu Ile Gln Ala Gln Met Asn Trp

206 50 55 60

209 Trp Gln Asp Gln Leu Lys Leu Met Gln His Thr Leu Leu Lys Ser Ala

210 65 70 75 80

213 Gly Gln Pro Ser Glu Pro Val Ile Thr Pro Glu Arg Ser Asp Arg Arg

214 85 90 95

217 Phe Lys Ala Glu Ala Trp Ser Glu Gln Pro Ile Tyr Asp Tyr Leu Lys

218 100 105 110

221 Gln Ser Tyr Leu Leu Thr Ala Arg His Leu Leu Ala Ser Val Asp Ala

222 115 120 125

225 Leu Glu Gly Val Pro Gln Lys Ser Arg Glu Arg Leu Arg Phe Phe Thr

226 130 135 140

229 Arg Gln Tyr Val Asn Ala Met Ala Pro Ser Asn Phe Leu Ala Thr Asn

230 145 150 155 160

233 Pro Glu Leu Leu Lys Leu Thr Leu Glu Ser Asp Gly Gln Asn Leu Val

234 165 170 175

237 Arg Gly Leu Ala Leu Leu Ala Glu Asp Leu Glu Arg Ser Ala Asp Gln

238 180 185 190

241 Leu Asn Ile Arg Leu Thr Asp Glu Ser Ala Phe Glu Leu Gly Arg Asp

242 195 200 205

245 Leu Ala Leu Thr Pro Gly Arg Val Val Gln Arg Thr Glu Leu Tyr Glu

246 210 215 220

249 Leu Ile Gln Tyr Ser Pro Thr Glu Thr Val Gly Lys Thr Pro Val

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250	225	230	235	240
253	Leu Ile Val Pro Pro Phe Ile Asn Lys Tyr Tyr Ile Met Asp Met Arg			
254	245	250	255	
257	Pro Gln Asn Ser Leu Val Ala Trp Leu Val Ala Gln Gly Gln Thr Val			
258	260	265	270	
261	Phe Met Ile Ser Trp Arg Asn Pro Gly Val Ala Gln Ala Gln Ile Asp			
262	275	280	285	
265	Leu Asp Asp Tyr Val Val Asp Gly Val Ile Ala Ala Leu Asp Gly Val			
266	290	295	300	
269	Glu Ala Ala Thr Gly Glu Arg Glu Val His Gly Ile Gly Tyr Cys Ile			
270	305	310	315	320
273	Gly Gly Thr Ala Leu Ser Leu Ala Met Gly Trp Leu Ala Ala Arg Arg			
274	325	330	335	
277	Gln Lys Gln Arg Val Arg Thr Ala Thr Leu Phe Thr Thr Leu Leu Asp			
278	340	345	350	
281	Phe Ser Gln Pro Gly Glu Leu Gly Ile Phe Ile His Glu Pro Ile Ile			
282	355	360	365	
285	Ala Ala Leu Glu Ala Gln Asn Glu Ala Lys Gly Ile Met Asp Gly Arg			
286	370	375	380	
289	Gln Leu Ala Val Ser Phe Ser Leu Leu Arg Glu Asn Ser Leu Tyr Trp			
290	385	390	395	400
293	Asn Tyr Tyr Ile Asp Ser Tyr Leu Lys Gly Gln Ser Pro Val Ala Phe			
294	405	410	415	
297	Asp Leu Leu His Trp Asn Ser Asp Ser Thr Asn Val Ala Gly Lys Thr			
298	420	425	430	
301	His Asn Ser Leu Leu Arg Arg Leu Tyr Leu Glu Asn Gln Leu Val Lys			
302	435	440	445	
305	Gly Glu Leu Lys Ile Arg Asn Thr Arg Ile Asp Leu Gly Lys Val Lys			
306	450	455	460	
309	Thr Pro Val Leu Leu Val Ser Ala Val Asp Asp His Ile Ala Leu Trp			
310	465	470	475	480
313	Gln Gly Thr Trp Gln Gly Met Lys Leu Phe Gly Gly Glu Gln Arg Phe			
314	485	490	495	
317	Leu Leu Ala Glu Ser Gly His Ile Ala Gly Ile Ile Asn Pro Pro Ala			
318	500	505	510	
321	Ala Asn Lys Tyr Gly Phe Trp His Asn Gly Ala Glu Ala Glu Ser Pro			
322	515	520	525	
325	Glu Ser Trp Leu Ala Gly Ala Thr His Gln Gly Gly Ser Trp Trp Pro			
326	530	535	540	
329	Glu Met Met Gly Phe Ile Gln Asn Arg Asp Glu Gly Ser Glu Pro Val			
330	545	550	555	560
333	Pro Ala Arg Val Pro Glu Glu Gly Leu Ala Pro Ala Pro Gly His Tyr			
334	565	570	575	
337	Val Lys Val Arg Leu Asn Pro Val Phe Ala Cys Pro Thr Glu Glu Asp			
338	580	585	590	
341	Ala Ala			
345	<210> SEQ ID NO: 6			
346	<211> LENGTH: 246			
347	<212> TYPE: PRT			

RAW SEQUENCE LISTING

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348 <213> ORGANISM: Ralstonia eutropha
 350 <400> SEQUENCE: 6
 352 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
 353 1 5 10 15
 356 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
 357 20 25 30
 360 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
 361 35 40 45
 364 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
 365 50 55 60
 368 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
 369 65 70 75 80
 372 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
 373 85 90 95
 376 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
 377 100 105 110
 380 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
 381 115 120 125
 384 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
 385 130 135 140
 388 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
 389 145 150 155 160
 392 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
 393 165 170 175
 396 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
 397 180 185 190
 400 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
 401 195 200 205
 404 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
 405 210 215 220
 408 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
 409 225 230 235 240
 412 Gly Gly Leu His Met Gly
 413 245
 416 <210> SEQ ID NO: 7
 417 <211> LENGTH: 2196
 418 <212> TYPE: DNA
 419 <213> ORGANISM: Artificial Sequence
 421 <220> FEATURE:
 422 <223> OTHER INFORMATION: chemically-synthesized ADE1 gene
 424 <400> SEQUENCE: 7
 425 taacagtatg atttttttcc ctctcccgcc gattgagggtt tttttttctt ctttcgcttt 60
 427 ggtctttgc ttttcactcc aaaaatggaa acacgcgcgg ctcaactcga aatccgtgat 120
 429 caaaaaaaaata aaggctgtga gtttcgagcc aataattatg aattagtggat atttttttta 180
 431 aagataaaata atcaagaatc gcatttaggaa gacgaatatg cgttattcaa ataaaaagac 240
 433 aattctttta gggtagcatt tcccttcaag ttcatcccac atgtacattaa atgtcaatga 300
 435 tgtcgagaa gttaaattag cagaagaaaa aaaaaatgtg aattactccg agtcaactct 360
 437 tctttctttt cttcttttc ttctttatca ccataatcac caccaccacc accaccacca 420
 439 gctcccgat gacttcaact aacttagaag gaactttccc attgattgcc aaaggtaaag 480

VERIFICATION SUMMARY

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Input Set : A:\Q96497 Sequence Listing.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date